

**Figure 1**

**85P1B3 SSH sequence and GenBank homology to OIP5**

GATCAGAGGACACATGGGACTCTGCATCTTAATTCTAAATTACAGTCAAAGACATTTCAG  
AGATAAGTATTATGAATTCAATAAGAACATCTAAAGTAAGTTCTTAAGGCAAATAGCTATAAAA  
GAGAAGAACATCCTAGTCTCATCTTCTAAAAACAGCTTCACAAATAATTGGAAAATCAGCC  
TAAAGGTAAATAGAAACTGCATTCCCCTCCATTCTTGAAGCCAATCTTTCAAGAAATGAC  
TAAGCAGCACCTGTTGAAGACAGCAATAAGCCTGAACCTGACACTCAAGCTTGTTACA  
GGATC

gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein... 632 e-179

gb|AF158642.1|AF158642 Homo sapiens metalloproteinase-disin... 42 0.12

gb|AC005075.2|AC005075 Homo sapiens clone RG219E16, complet... 42 0.12

emb|AL096773.6|HS1000E10 Human DNA sequence from clone 1000... 40 0.48

>gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein OIP5 mRNA, partial cds  
Length = 1197

Score = 632 bits (319), Expect = e-179

Identities = 319/319 (100%)

Strand = Plus / Minus

Query: 1 gatcagaggacacatgggactctgcattttaattcctaaattttacagtcaaagacatttt 60  
|||||||  
Sbjct: 1013 gatcagaggacacatgggactctgcattttaattcctaaattttacagtcaaagacatttt 954

Query: 61 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatacgta 120  
|||||||  
Sbjct: 953 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatacgta 894

Query: 121 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataattggaa 180  
|||||||  
Sbjct: 893 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataattggaa 834

Query: 181 aatcagcctaaggtaaatagaaactgcattccctccattttgaagccaatctttt 240  
|||||||  
Sbjct: 833 aatcagcctaaggtaaatagaaactgcattccctccattttgaagccaatctttt 774

Query: 241 caagaaatgactaaggcagcacctgttgttgaagacagcaataagcctgaacctgacact 300  
|||||||  
Sbjct: 773 caagaaatgactaaggcagcacctgttgttgaagacagcaataagcctgaacctgacact 714

Query: 301 caagcttggtagggatc 319  
|||||||  
Sbjct: 713 caagcttggtagggatc 695

**Figure 2**

**cDNA Sequence and ORF of 85P1B3/OIP5 clone A**

5'	<pre>       9       18       27       36       45       54       GGC TGC <b>GGG AAG ATG</b> GCG GCT CAG CCG CTG CGG CAT CGC TCA CGT TGT GCA ACG       ----- -----       M A A Q P L R H R S R C A T       63       72       81       90       99       108       CCG CCC CGG GGG GAC TTT TGT GGT GGC ACT GAG AGG GCG ATT GAC CAA GCT TCT       ----- -----       P P <b>R G D</b> F C G G T E R A I D Q A S       117      126      135      144      153      162       TTT ACG ACC TCC ATG GAG TGG GAT ACG CAG GTG GTG AAG GGG TCC TCG CCG CTC       ----- -----       F T T S M E W D T Q V V K G S S P L       171      180      189      198      207      216       GGC CCC GCA GGG CTG GGG GCT GAG GAG CCA GCC GCC GGC CCG CAG CTG CCG TCT       ----- -----       G P A G L G A E E P A A G P Q L P S       225      234      243      252      261      270       TGG CTG CAG CCT GAG AGG TGC GCT GTG TTC CAG TGC GCA CAG TGT CAC GCA GTG       ----- -----       W L Q P E R C A V F Q C A Q C H A V       279      288      297      306      315      324       CTC GCC GAC TCG GTG CAC CTC GCC TGG GAC CTG TCG CGG TCC CTC GGG GCC GTG       ----- -----       L A D S V H L A W D L S R S L G A V       333      342      351      360      369      378       GTC TTC TCC AGA GTT ACA AAT AAC GTC GTT TTG GAA GCG CCC TTC CTA GTT GGC       ----- -----       V F S R V T N N V V L E A P F L V G       387      396      405      414      423      432       ATT GAA GGT TCA CTC AAA GCC AGT ACT TAC AAC CTT TTA TTC TGT GGT TCT TGT       ----- -----       I E G S L K G S T Y N L L F C G S C       441      450      459      468      477      486       GGG ATT CCC GTT GGT TTC CAT CTG TAT TCT ACC CAT GCT GCC CTG GCT GCC TTG       ----- -----       G I P V G F H L Y S T H A A L A A L       495      504      513      522      531      540       AGA GGT CAC TTC TGC CTT TCC AGT GAC AAA ATG GTG TGC TAT CTC TTA AAA ACA       ----- -----       R G H F C L S S D K M V C Y L L K T       549      558      567      576      585      594       AAA GCC ATA GTA AAT GCA TCA GAG ATG GAT ATT CAA AAT GTT CCT CTA TCA GAA       ----- -----       K A I V N A S E M D I Q N V P L S E       603      612      621      630      639      648       AAG ATT GCA GAG CTG AAA GAG AAG ATA GTG CTA ACG CAC AAT CGC TTA AAA TCA       ----- -----       K I A E L K E K I V L T H N R L K S     </pre>
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Title: Title: NUCLEIC ACID AND CORRESPONDING  
Inventor(s): Arthur B. RAITANO  
Application No.: Currently unknown  
Docket No.: 511582002800

Sheet 4 of 22

**Figure 3**

**85P1B3/OIP5 protein sequence.**

```
1 MAAQPLRHRS RCATPPRGDF CGGTERAIDQ ASFTTSMEWWD TQVVKGSSPL GPAGLGAEFP
61 AAGPQLPSWL QPERCAVFQC AQCHAVLADS VHLAWDLRSRS LGAVVFSRVT NNVVLEAPFL
121 VGIEGSLKGS TYNLLFCGSC GIPVGFHLYS THAALAALRG HFCLSSDKMV CYLLKTKAIV
181 NASEMDIQNV PLSEKIAELK EKIVLTHNRL KSLMKILSEV TPDQSKPEN*
```

**Figure 4**

Alignment of 85P1B3 with OIP5.

>gi|2815610|gb|AAC39561.1| (AF025441) Opa-interacting protein OIP5 [Homo sapiens]  
Length = 231

Score = 462 bits (1189), Expect = e-130

Identities = 229/229 (100%), Positives = 229/229 (100%)

85P1B3:	1	MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP	60
		MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP	
OIP5:	3	MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP	62
85P1B3:	61	AAGPQLPSWLQPERCAVFQCAQCHA VLADSVHLAWDLSRS LGA VVFSRV TNNV LEAPFL	120
		AAGPQLPSWLQPERCAVFQCAQCHA VLADSVHLAWDLSRS LGA VVFSRV TNNV LEAPFL	
OIP5:	63	AAGPQLPSWLQPERCAVFQCAQCHA VLADSVHLAWDLSRS LGA VVFSRV TNNV LEAPFL	122
85P1B3:121		VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHA ALAALRGHFCLSSDKMVCYLLKTAIV	180
		VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHA ALAALRGHFCLSSDKMVCYLLKTAIV	
OIP5:	123	VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHA ALAALRGHFCLSSDKMVCYLLKTAIV	182
85P1B3:181		NASEMDIQNVLSEKIAELKEKIVLTHNRLKSLMKIL SEVT PDQSKPEN	229
		NASEMDIQNVLSEKIAELKEKIVLTHNRLKSLMKIL SEVT PDQSKPEN	
OIP5:	183	NASEMDIQNVLSEKIAELKEKIVLTHNRLKSLMKIL SEVT PDQSKPEN	231

PROTEIN ALIGNMENT

Figure 5: 85P1B3 Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

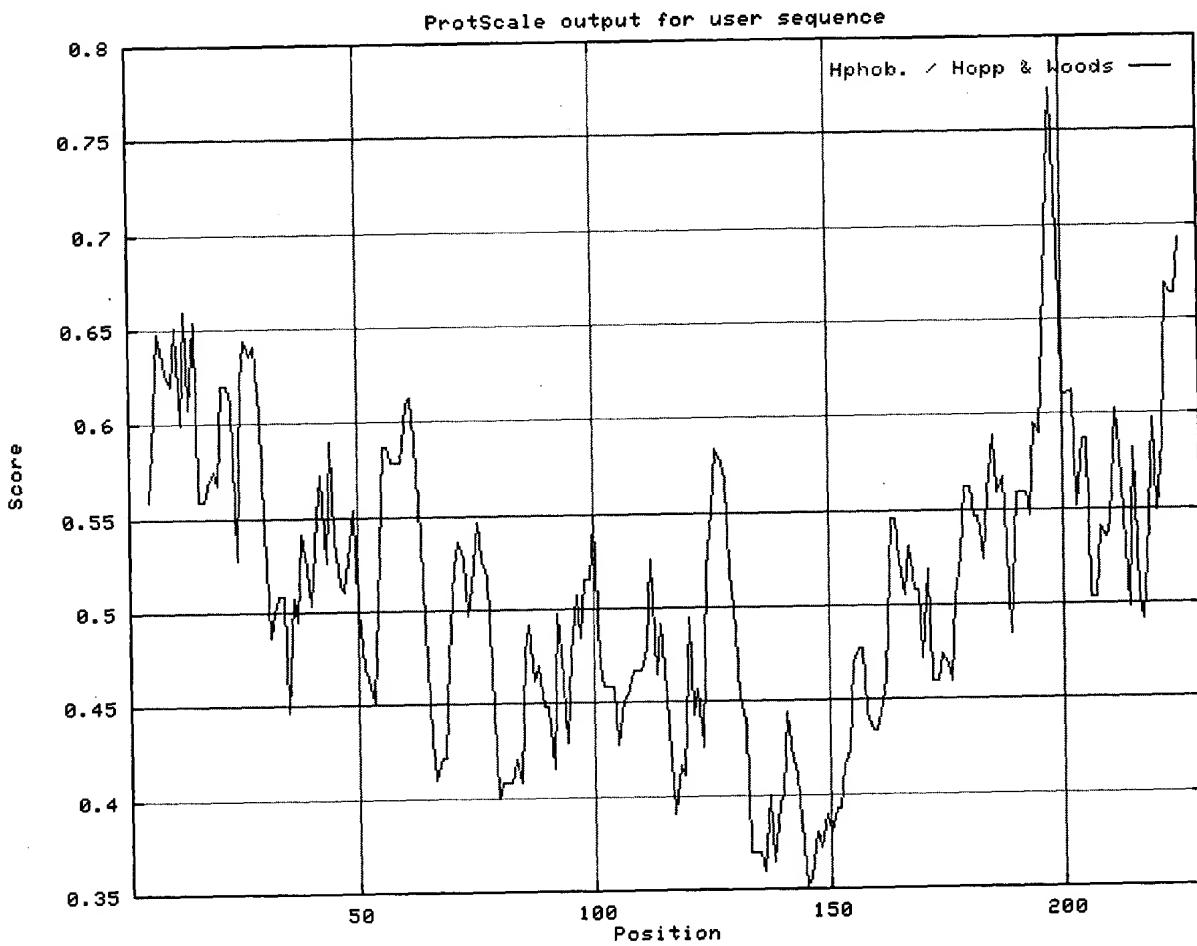


Figure 6: 85P1B3 Hydropathicity Profile  
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

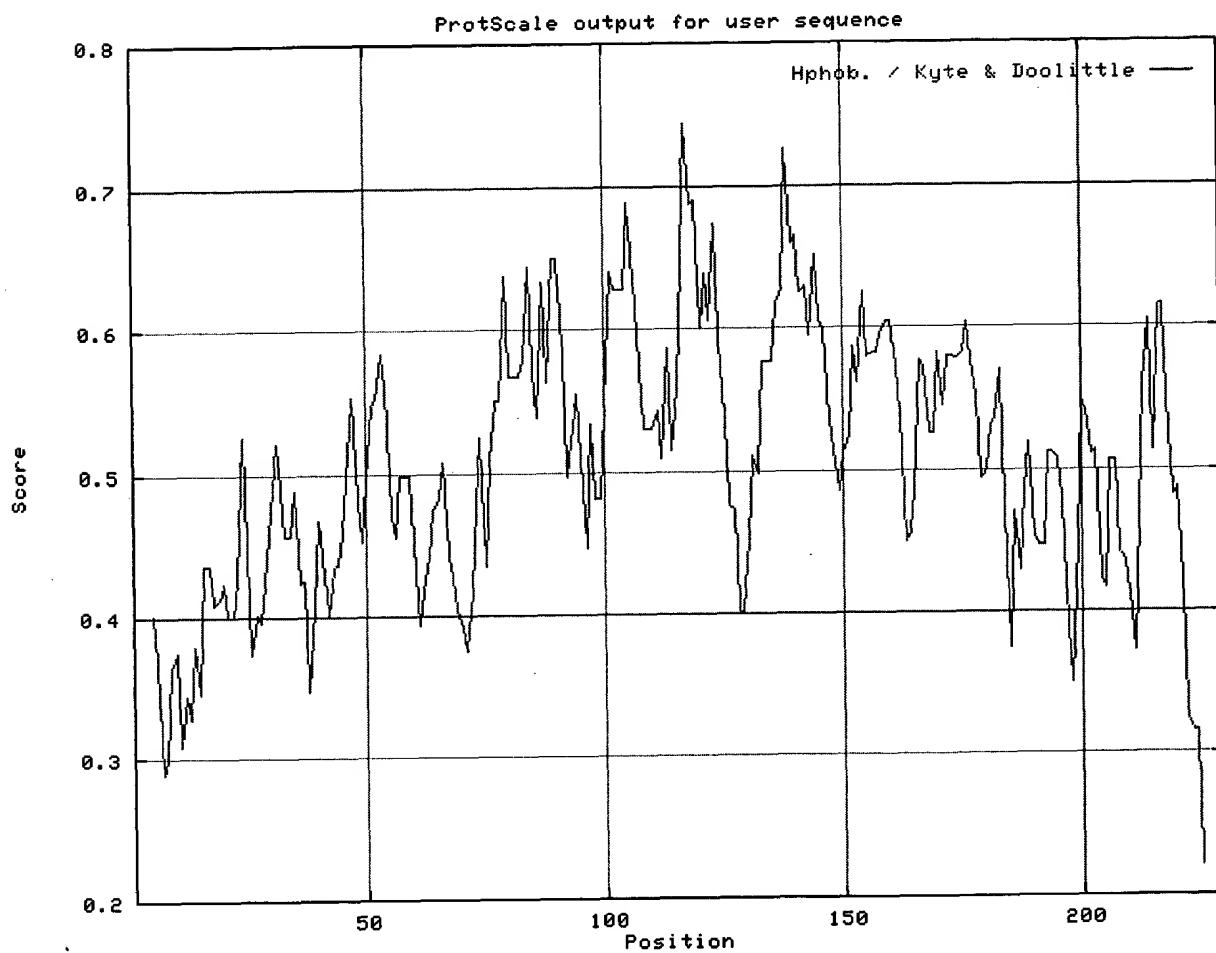


Figure 7: 85P1B3 % Accessible Residues Profile  
(Janin J., 1979. Nature 277:491-492)

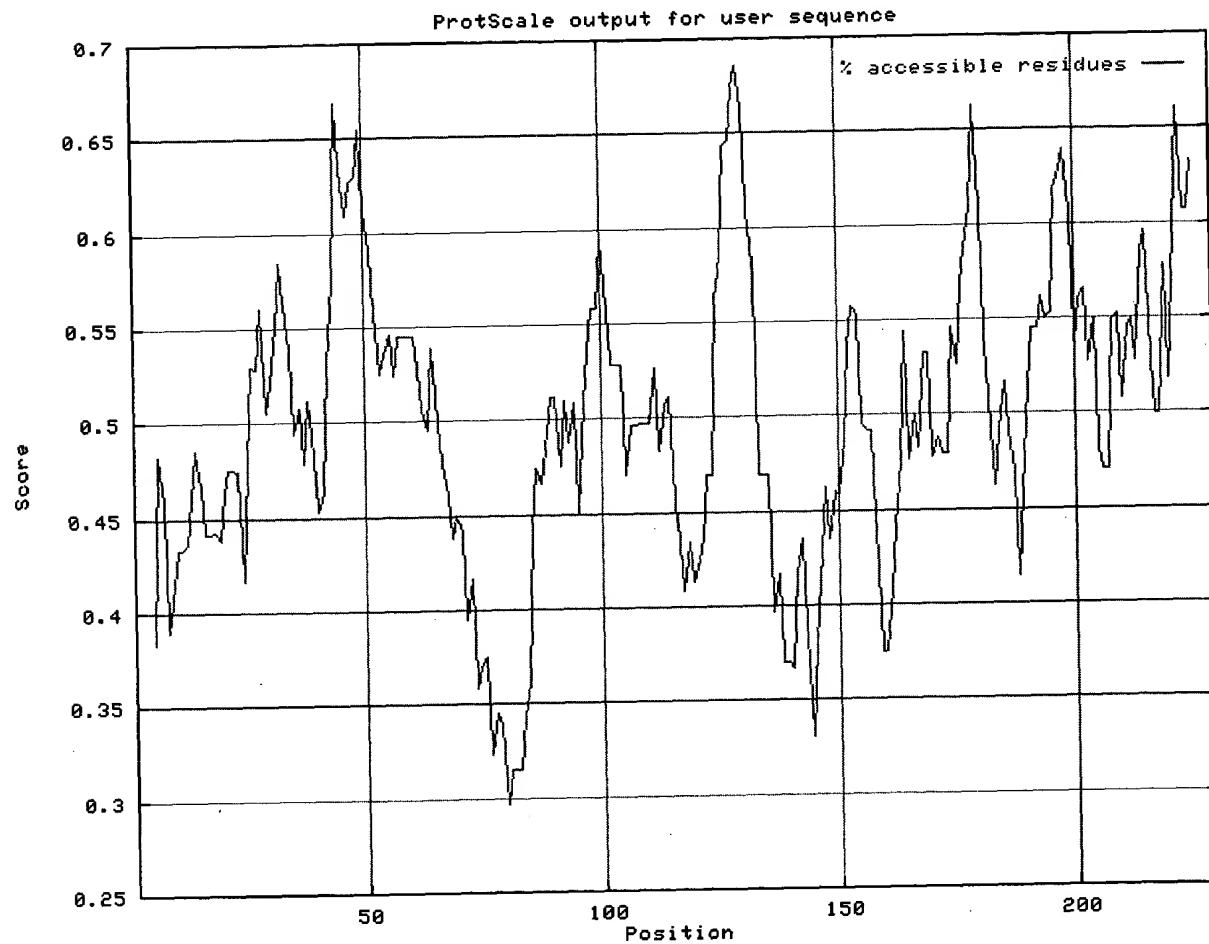


Figure 8: 85P1B3 Average Flexibility Profile  
(Bhaskaran R., Ponnuswamy P.K., 1988.  
Int. J. Pept. Protein Res. 32:242-255)

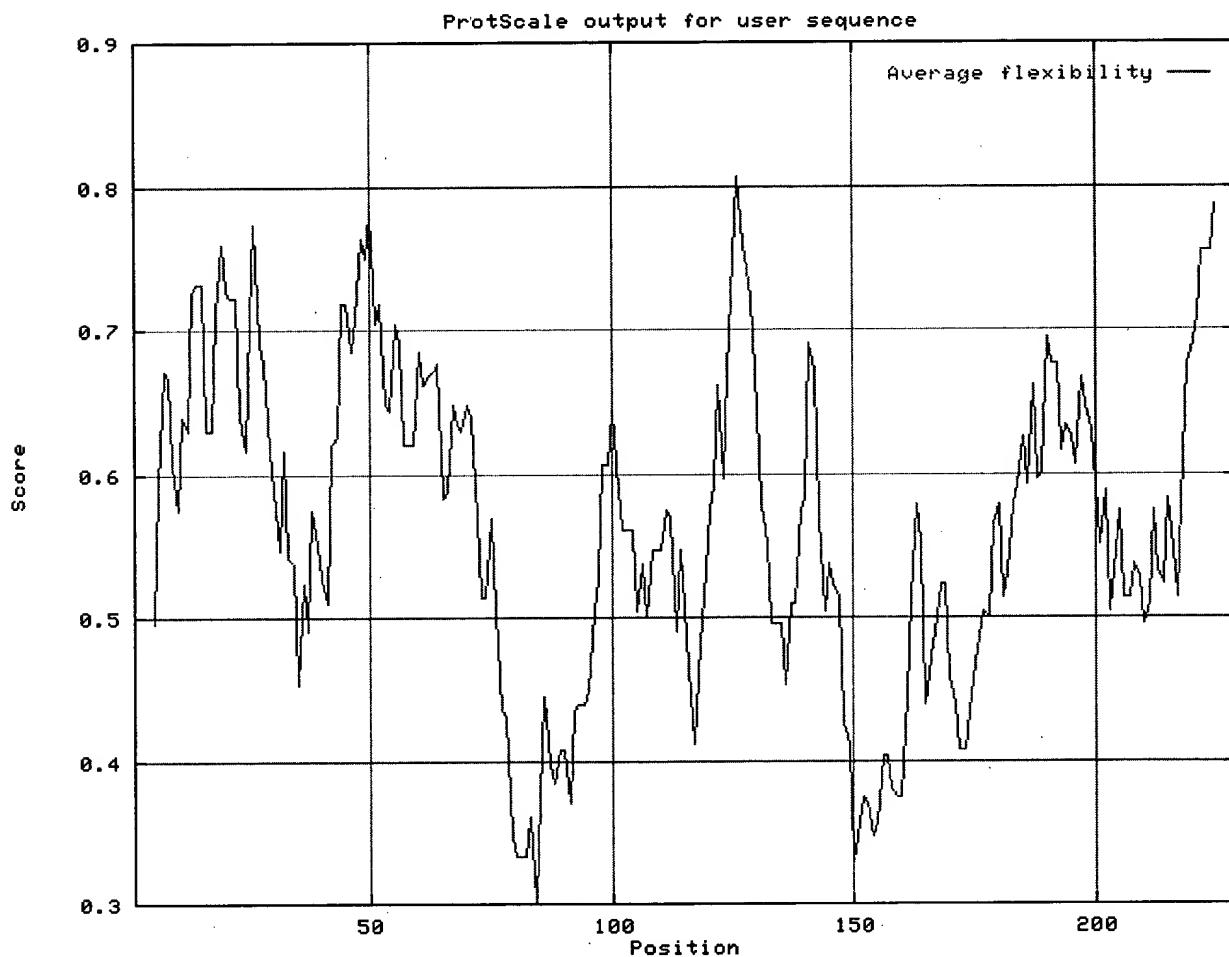
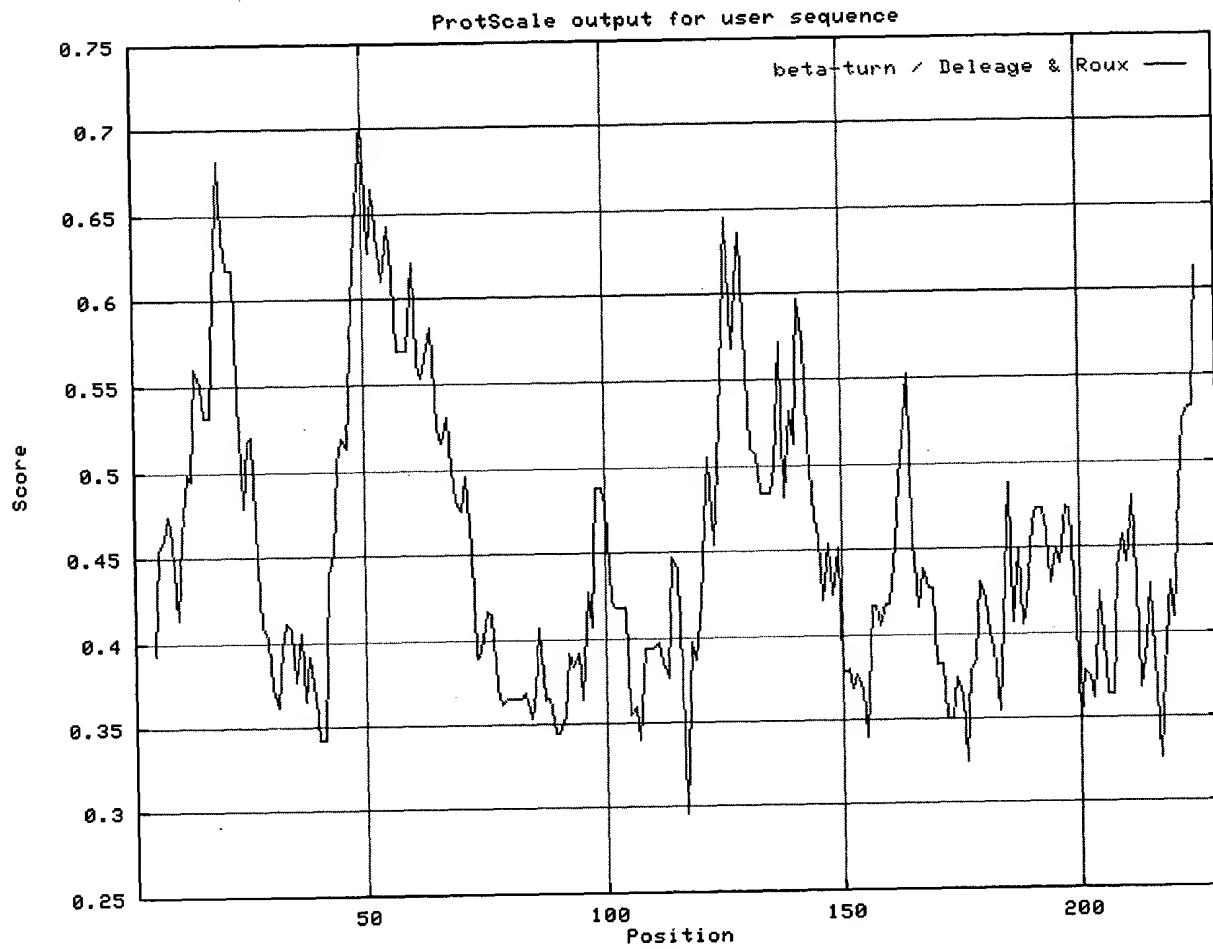
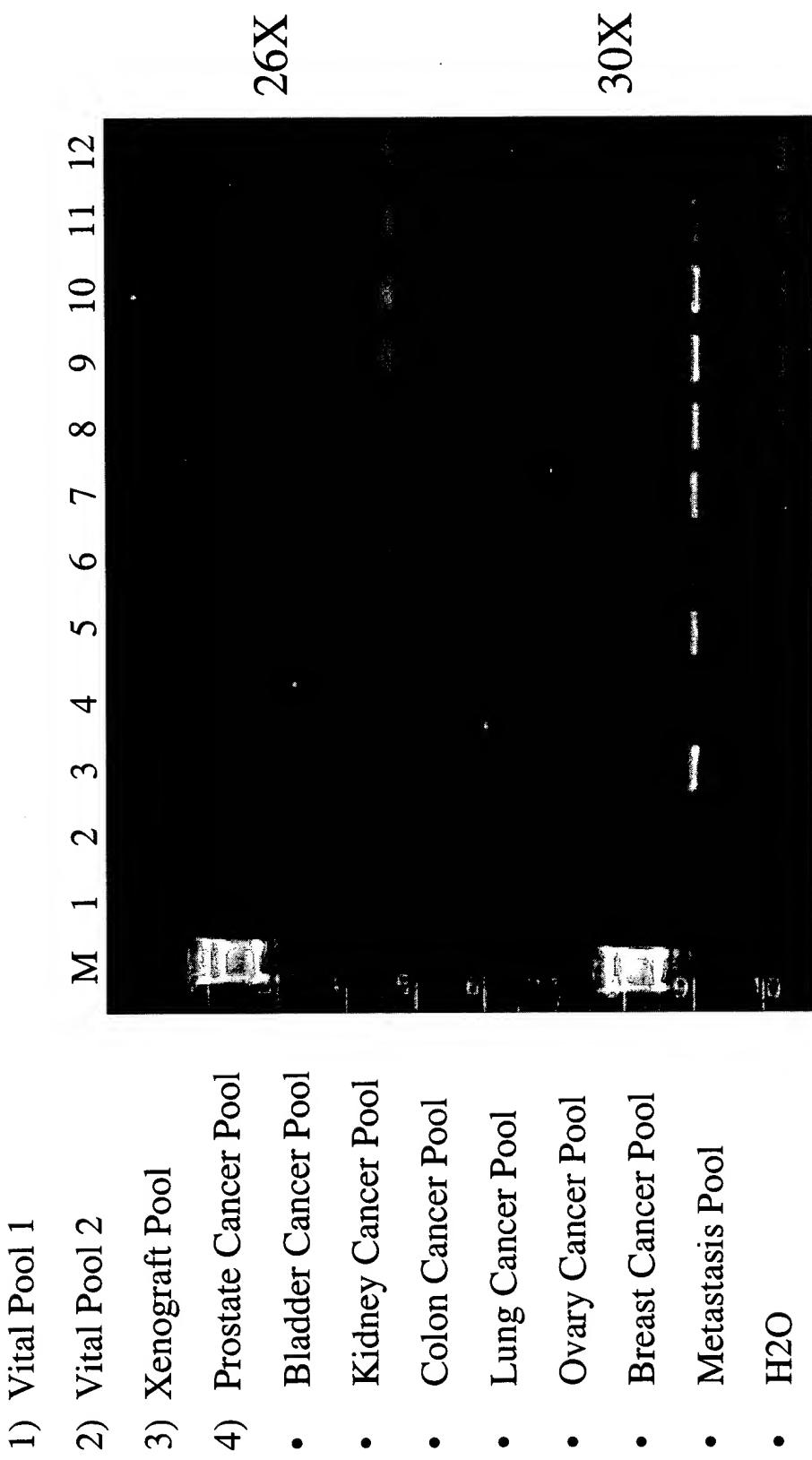


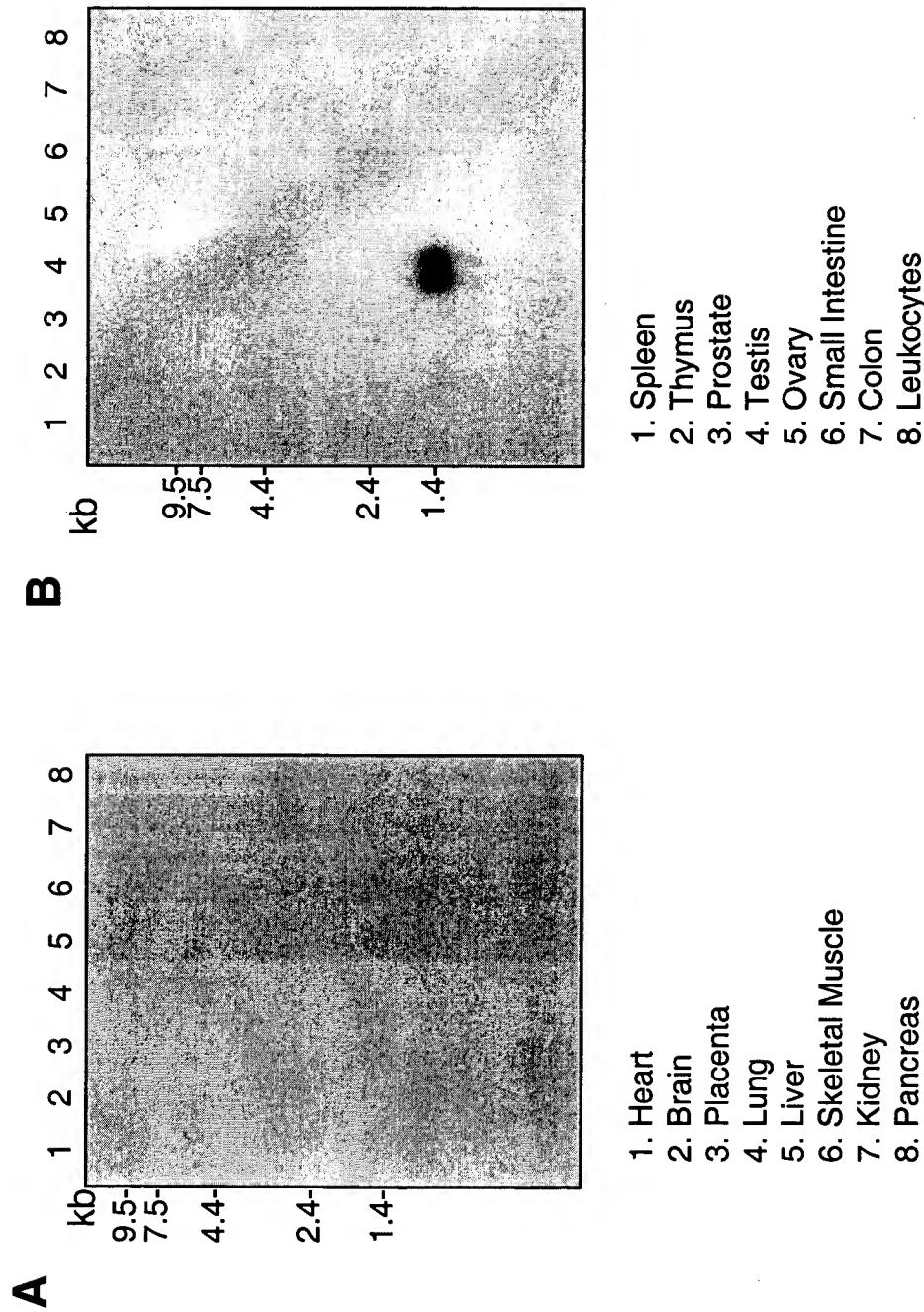
Figure 9: 85P1B3 Beta-turn Profile  
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)



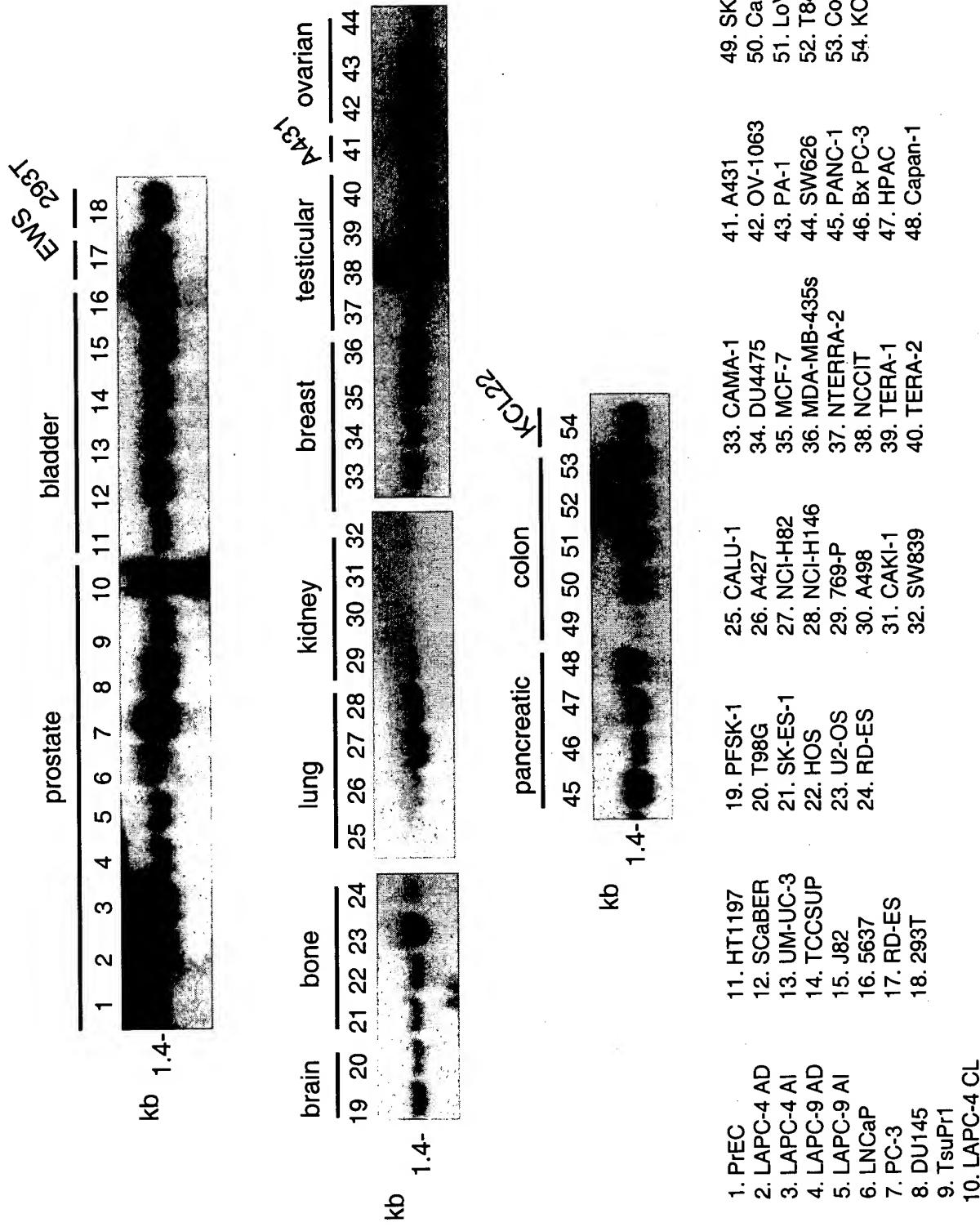
**Figure 10** RT-PCR analysis of 85P1B3 expression.



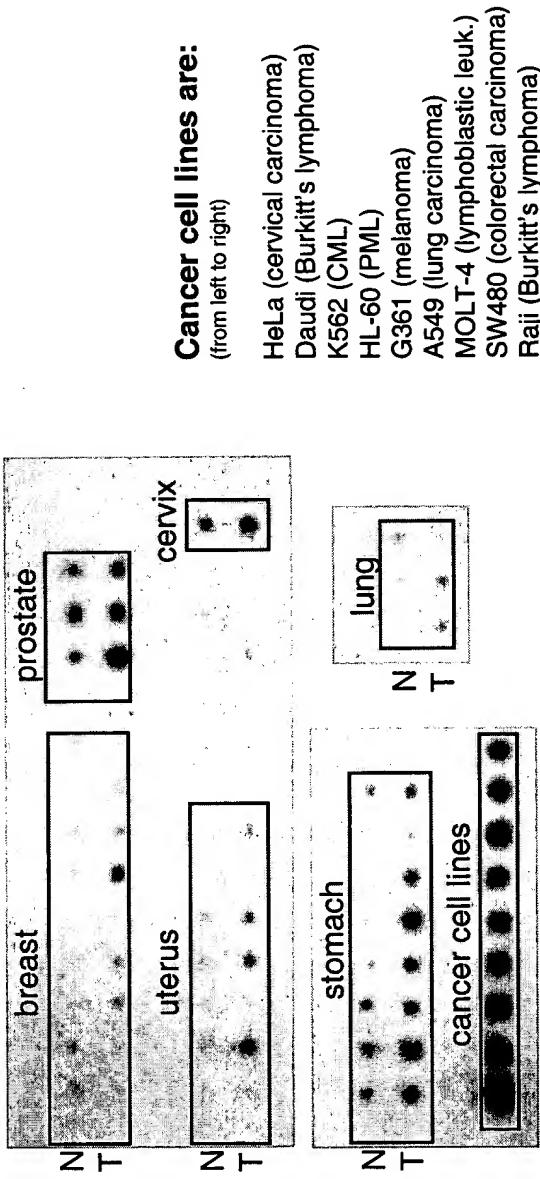
**Figure 11** Expression of 85P1B3 in Normal Human Tissues



**Figure 12 Expression of 85P1B3 in Human Cancer Cell lines**

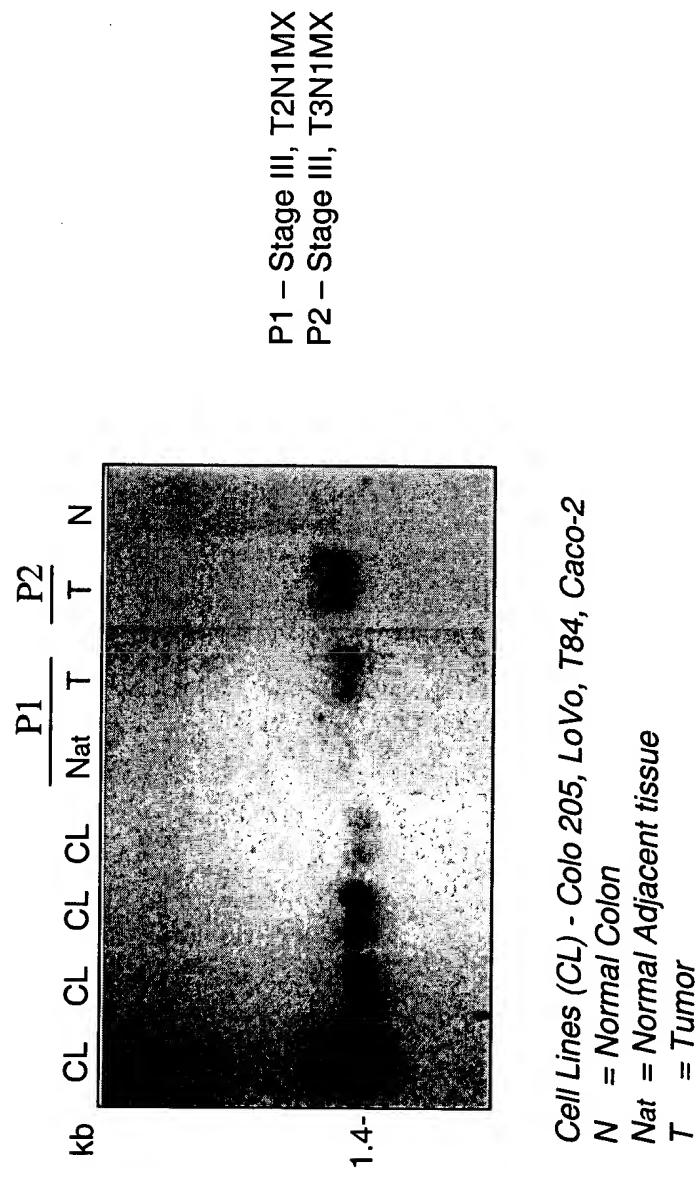


## Figure 13 Expression of 85P1B3 in Patient Cancer Specimens and Cancer Cell Lines

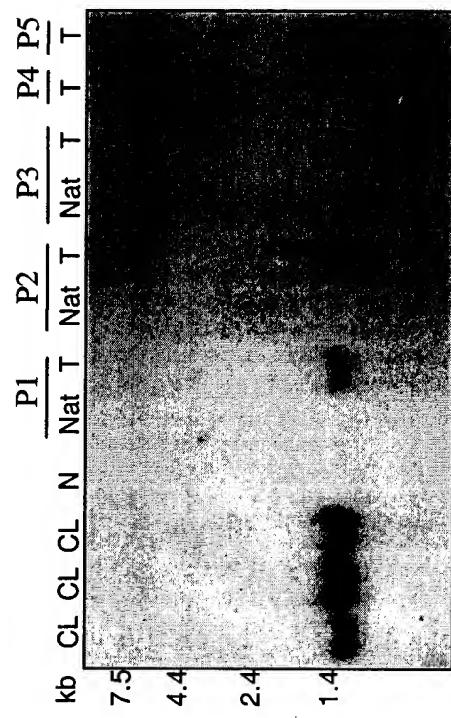


T = tumor RNA  
N = normal adjacent tissue RNA

**Figure 14** Expression of 85P1B3 in Colon Cancer Patient Specimens



**Figure 15 Expression of 85P1B3 in Bladder Cancer Patient Specimens**

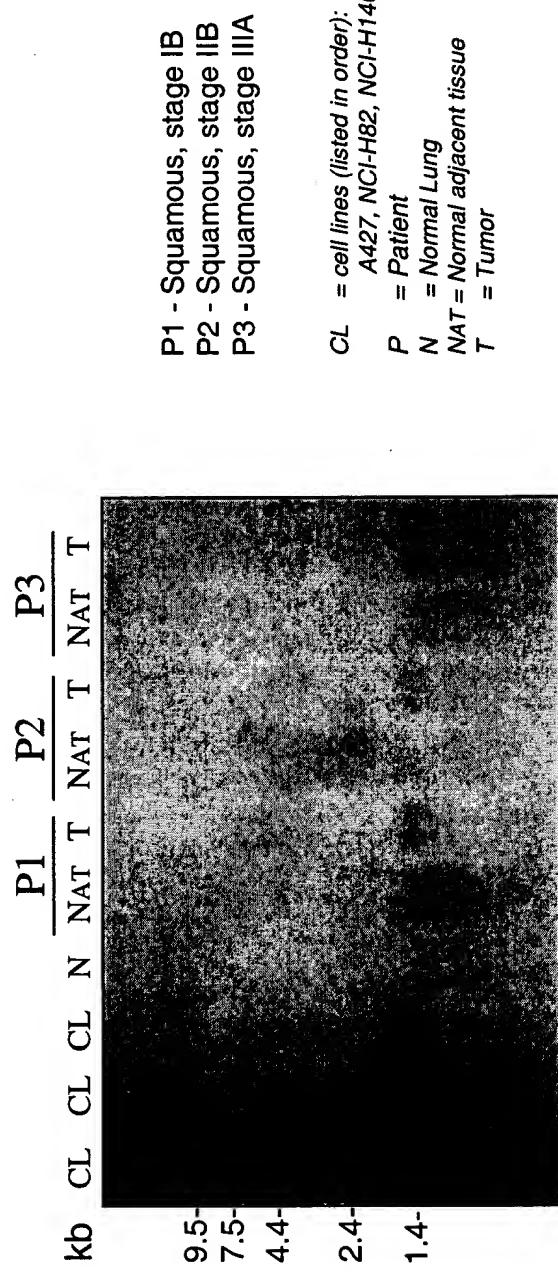


P1 - Transitional, grade 2  
P2 - Transitional, grade 3/2  
P3 - Transitional

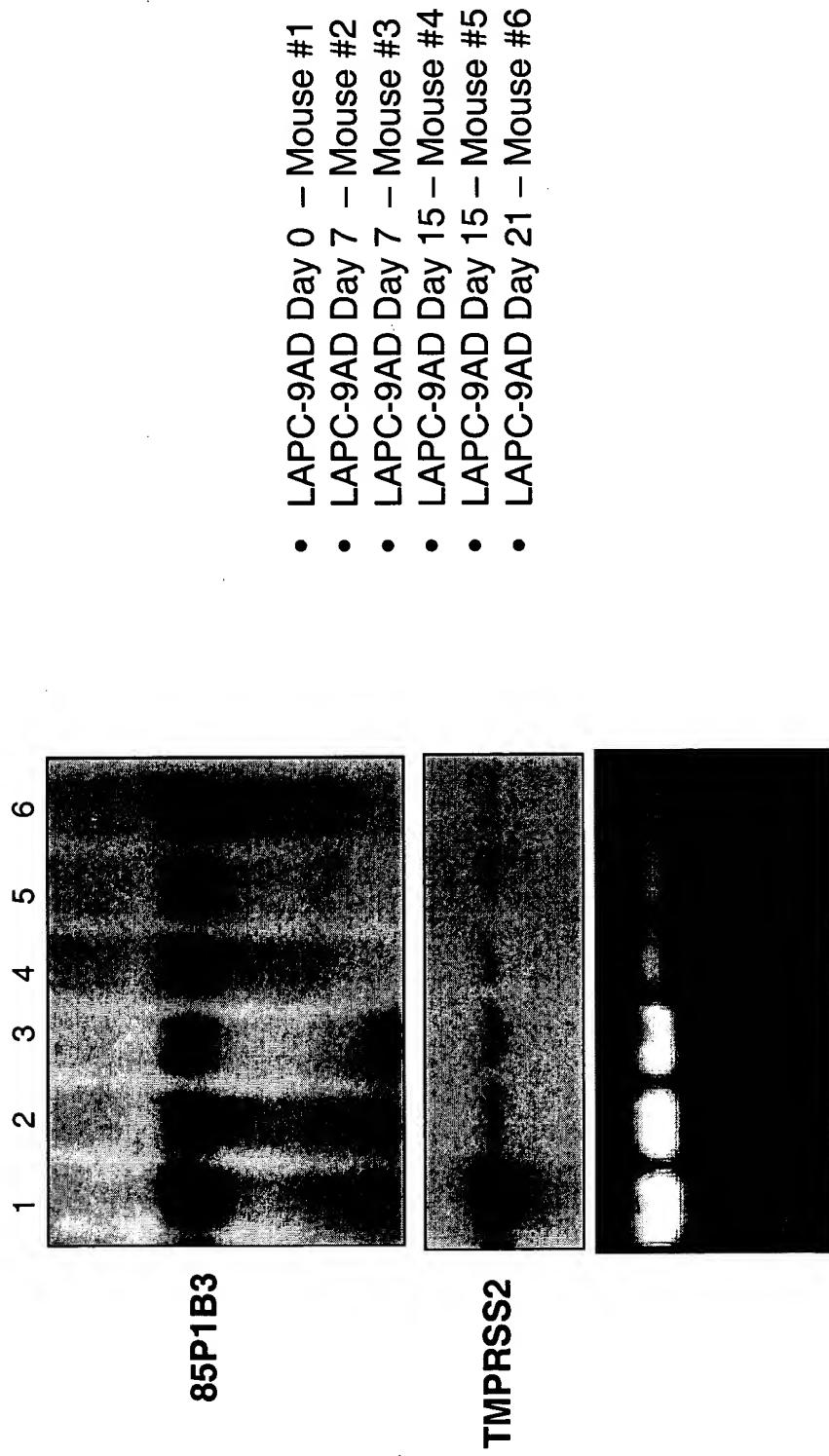
P4 - Polypoid cystitis  
P5 - Papillary, grade 3

C1 = cell lines listed in order: U/M-UC-3, J82, SCABER  
P = Patient  
N = Normal Bladder  
Nat = Normal adjacent tumor  
T = Tumor

**Figure 16 Expression of 85P1B3 in Lung Cancer Patient Specimens**



**Figure 17 Expression of 85P1B3 in Prostate Cancer Xenografts Following Castration**



**Figure 18 Expression of 85P1B3 in PC3 Cells Following Retroviral-Mediated Gene Delivery**

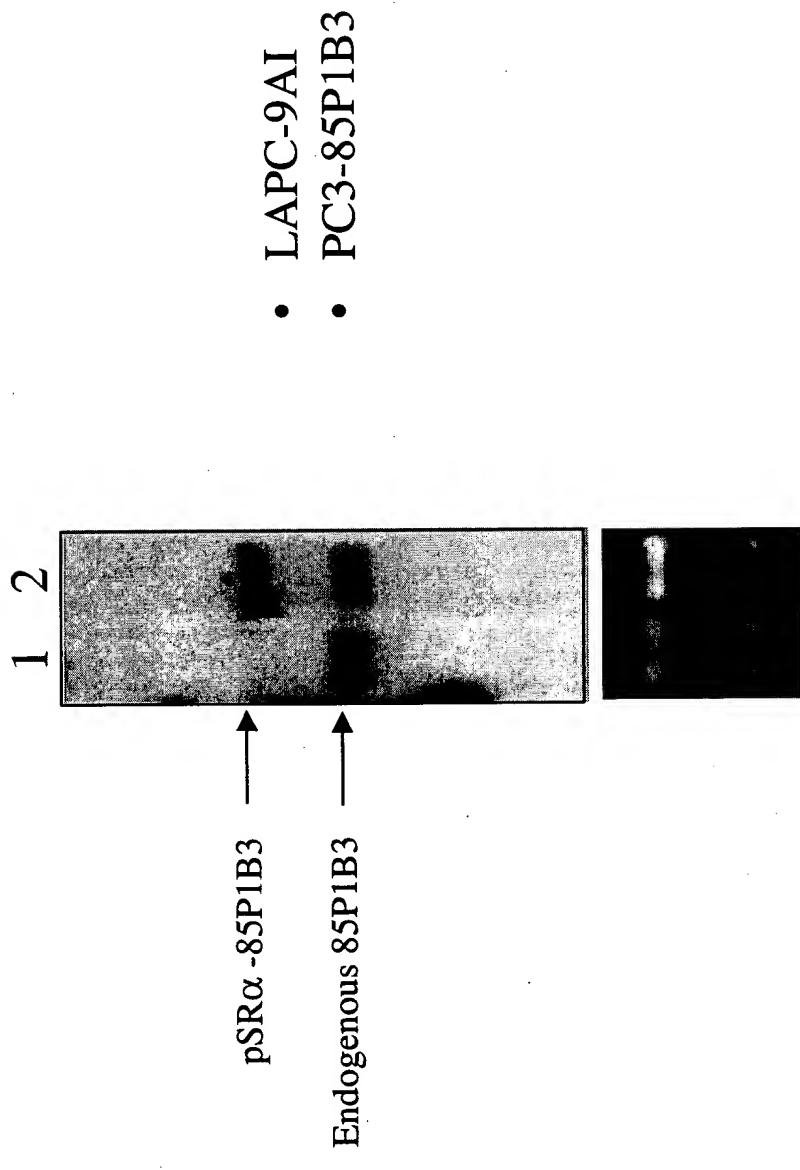
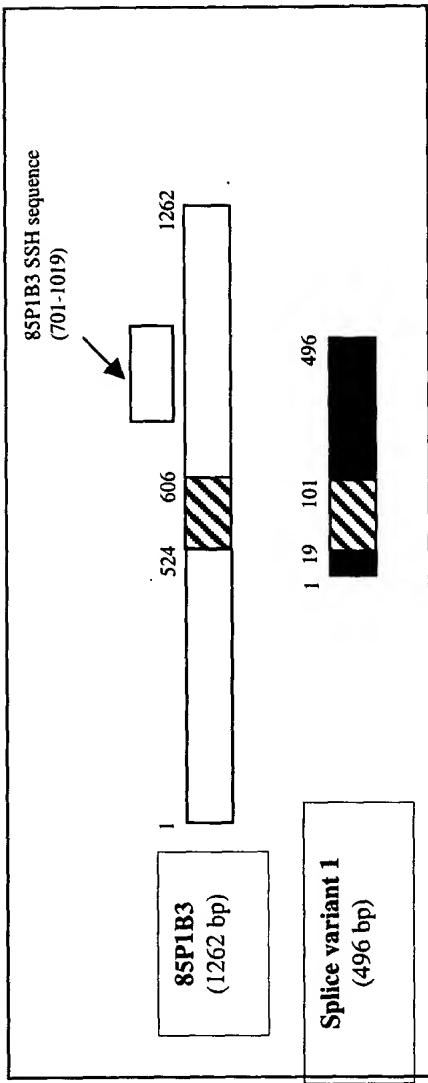
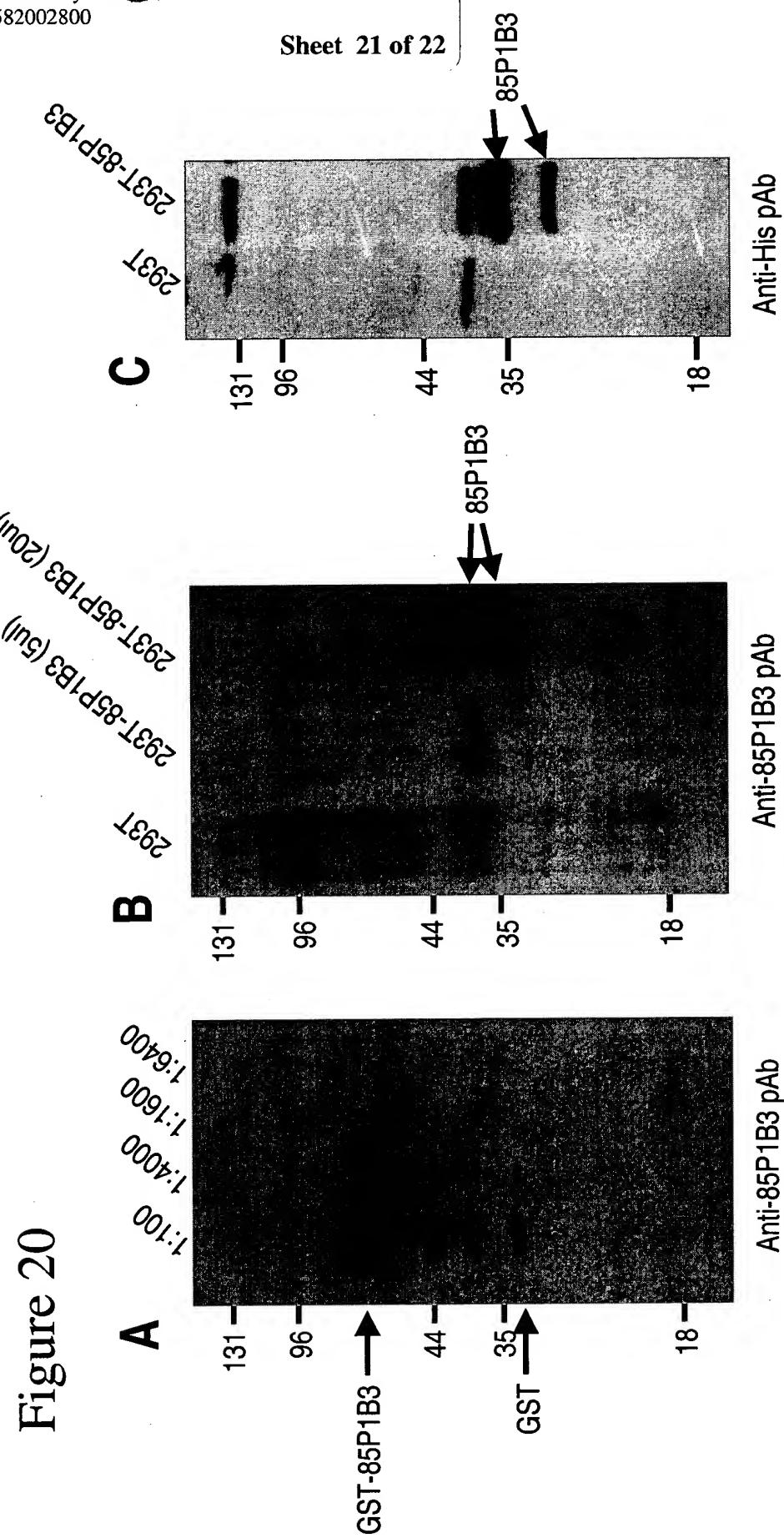
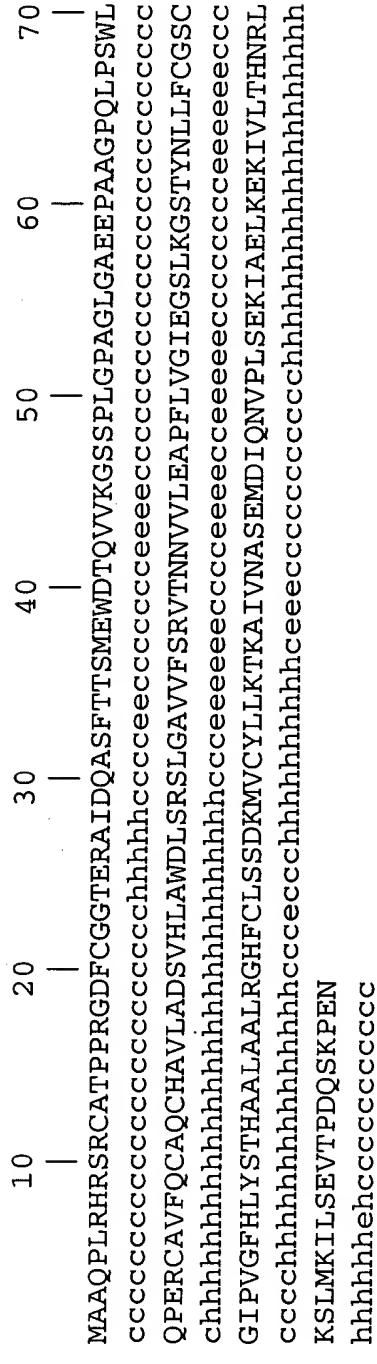


Figure 19.

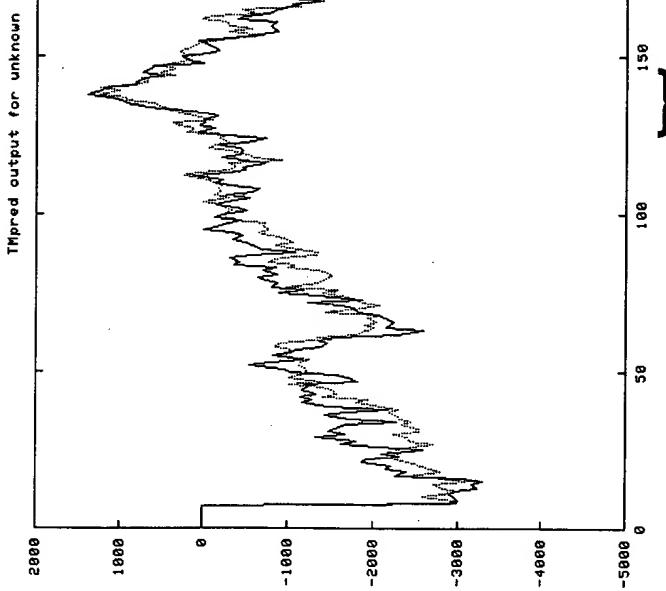




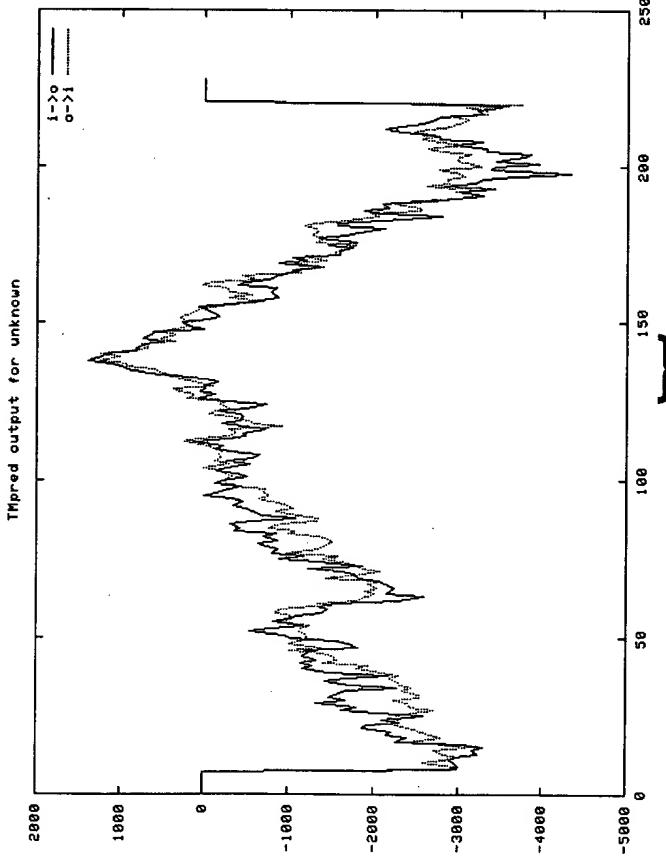
**Fig. 21A**



**Fig. 21B**



**Fig. 21C**



1 transmembrane from amino acids 129-149

No transmembrane domains, soluble protein

